

## CLAIMS

1. (Original) A method of obtaining information about a chemically active area of a target molecule, comprising:
  - providing a set of substantially rigid chemical gauges;
  - reacting said target with a plurality of gauges of said set of gauges;
  - assaying a binding of said gauges with said target to obtain a plurality of assay results;and
  - analyzing said assay results to obtain information about said chemically active area.
2. (Original) A method according to claim 1, wherein said gauges allow rotation of moieties of said gauges.
3. (Original) A method according to claim 1, wherein said gauges are constructed using a rigid scaffold.
4. (Original) A method according to claim 1, wherein constituent atoms of said gauges do not move more than 1 Å unless at least 20Kcal/Mol are applied to the gauge.
5. (Original) A method according to claim 1, wherein analyzing comprises identifying a plurality of spatial and chemically specific bindings configurations in said target active area.
6. (Original) A method according to claim 5, wherein said configurations comprise triangular configurations.
7. (Original) A method according to claim 5, wherein identifying comprises identifying a configuration that matches a configuration of a bound gauge.
8. (Original) A method according to claim 5, wherein identifying comprises identifying a configuration that does not match a configuration of a bound gauge.
9. (Original) A method according to claim 8, wherein identifying comprises identifying by statistical analysis of said assay results.

10. (Original) A method according to claim 9, wherein identifying comprises identifying by clustering.
11. (Original) A method according to claim 5, wherein identifying comprises assuming each gauge indicates a single configuration.
12. (Original) A method according to claim 5, wherein identifying comprises assuming at least some of the gauges indicate a plurality of configurations.
13. (Original) A method according to claim 5, wherein identifying comprises classifying gauges by chemical moieties at vertexes of said configurations.
14. (Original) A method according to claim 1, comprising reconstructing a spatial map of at least part of said chemically active area, from at least two of said assay results, said part including at least four chemical binding areas.
15. (Original) A method according to claim 14, wherein said part includes at least six chemical binding areas.
16. (Original) A method according to claim 5, comprising reconstructing a spatial map of at least part of said chemically active area, from at least two of configurations, said part including at least four chemical binding points.
17. (Original) A method according to claim 16, wherein said part includes at least six chemical binding areas.
18. (Original) A method according to claim 16, wherein reconstructing comprises:  
test-reconstructing a plurality of spatial maps from said configurations;  
scoring said maps; and  
selected a spatial map based on its score.
19. (Original) A method according to claim 16, wherein reconstructing comprises:

test-reconstructing a plurality of spatial maps from said configurations;  
clustering said maps according to common substructures; and  
selected a spatial map based on a relative property of a cluster it belongs to.

20. (Original) A method according to claim 19, wherein said relative property comprises size.
21. (Original) A method according to claim 16, wherein said spatial map includes enough binding points to ensure binding of a small molecule drug having a chemical profile matching the binding points.
22. (Original) A method according to claim 21, wherein said spatial map includes at least 6 binding points.
23. (Original) A method according to claim 21, wherein said spatial map includes at least 8 binding points.
24. (Original) A method according to claim 1, wherein said set of gauges comprises a set of gauges with at least 10,000 gauges.
25. (Original) A method according to claim 1, wherein said set of gauges comprises a set of gauges with at least 50,000 gauges.
26. (Original) A method according to claim 1, wherein said gauges comprise moieties arranged in spatial configurations and wherein said gauges are selected to span a virtual space of spatial chemical configurations.
27. (Original) A method according to claim 1, wherein substantially each point of virtual space that is spanned by said gauges is covered by at least two gauges.
28. (Original) A method according to claim 1, wherein substantially each point of virtual space that is spanned by said gauges is covered by at least three gauges.

29. (Original) A method according to claim 1, wherein at least 0.5% of said gauges bind with said target.
30. (Original) A method according to claim 1, wherein at least 1% of said gauges bind with said target.
31. (Original) A method according to claim 1, wherein at least 3% of said gauges bind with said target.
32. (Original) A method according to claim 1, wherein at least 50% of said gauges are defined by adding moieties to a set of fewer than 100 scaffolds.
33. (Original) A method according to claim 1, wherein at least 50% of said gauges are defined by adding moieties to a set of fewer than 50 scaffolds.
34. (Original) A method according to claim 1, wherein at least said set of gauges uses fewer than 15 different chemical moieties to define the chemical behavior of said gauges.
35. (Original) A method according to claim 1, wherein at least said set of gauges uses fewer than 10 different chemical moieties to define the chemical behavior of said gauges.
36. (Original) A method according to claim 1, wherein said assay is a functional assay.
37. (Original) A method according to claim 1, wherein said assay is a binding assay.
38. (Original) A method according to claim 1, wherein said assay is a cellular assay.
39. (Original) A method according to claim 1, wherein said assay is a flow-through assay.
40. (Original) A method according to claim 36, wherein said functional assay is performed in the presence of a natural substrate of said target.

41. (Original) A method according to claim 1, wherein said target comprises a protein including a biochemically active area adapted to engage a substrate.
42. (Original) A method according to claim 41, wherein said chemically active area comprises an area including said biochemically active area.
43. (Original) A method according to claim 41, wherein said chemically active area comprises a control area of said protein.
44. (Original) A method according to claim 1, analyzing comprises analyzing successful binding of at least 60 gauges.
45. (Original) A method according to claim 1, analyzing comprises analyzing successful binding of at least 10 gauges.
46. (Original) A method according to claim 1, analyzing comprises analyzing successful binding of at least 100 gauges.
47. (Original) A method according to claim 5, wherein identifying comprises identifying at least 40 different configurations.
48. (Original) A method according to claim 5, wherein identifying comprises identifying at least 10 different configurations.
49. (Original) A method according to claim 5, wherein identifying comprises identifying at least 100 different configurations.
50. (Original) A method according to claim 16, comprising:  
comparing said map to a lead data base; and  
selecting a lead from said data base for further use responsive to a semblance or lack of semblance between said lead and said map.
51. (Original) A method according to claim 16, comprising:

comparing said map to a lead data base; and  
rejecting a lead from said data base for further use responsive to a semblance between  
said lead and said map.

52. (Original) A method according to claim 16, comprising:  
constructing a lead to have a semblance to said map.

53. (Original) A method according to claim 52, wherein constructing comprises  
constructing using said gauges or scaffolds used to define said gauges.

54. (Original) A method according to claim 5, comprising:  
comparing said configurations to a lead data base; and  
selecting a lead from said data base for further use responsive to a matching of said  
configurations to said lead.

55. (Original) A method according to claim 5, comprising:  
constructing a lead based on said configurations.

56. (Original) A method according to claim 5, comprising:  
selecting at least one of said gauges as a lead for drug discovery.

57. (Original) A method according to claim 1, comprising comparing the binding of gauges  
with similar binding geometries to obtain steric clashing data; and  
analyzing said steric clashing data to provide geometrical information about said target.

58. – 101. (Cancelled)

102. (Original) A method according to claim 1, comprising generating a set of drug leads for  
said target based on said information.

103. (Original) A method according to claim 102, comprising removing known drug leads  
for said target from said set.

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104. – 154. (Cancelled)